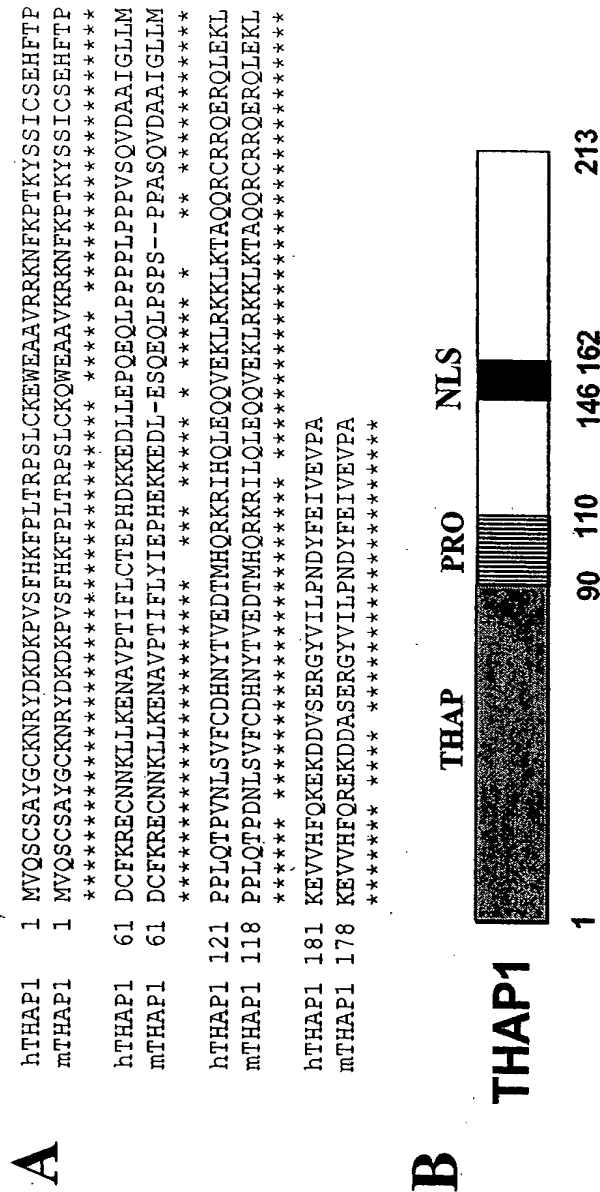


FIGURE 1



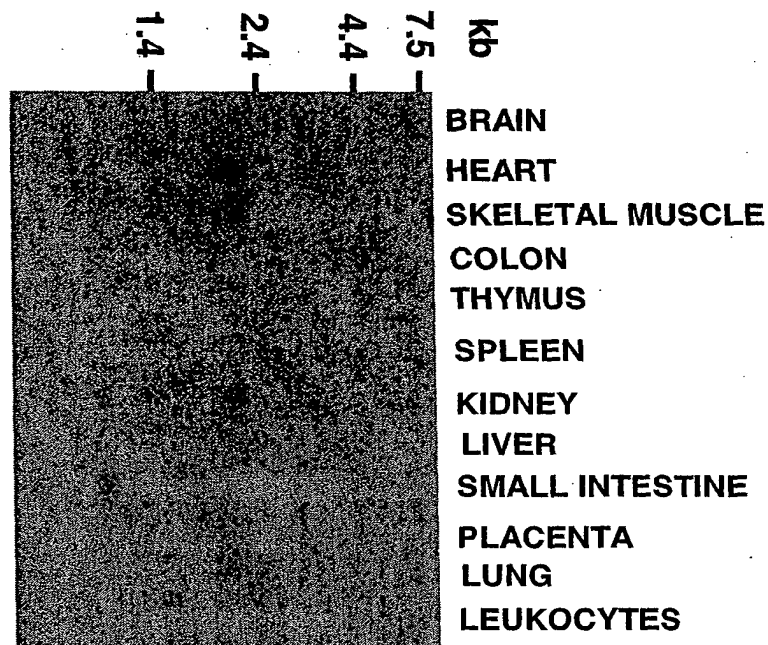


FIGURE 2

Figure 3

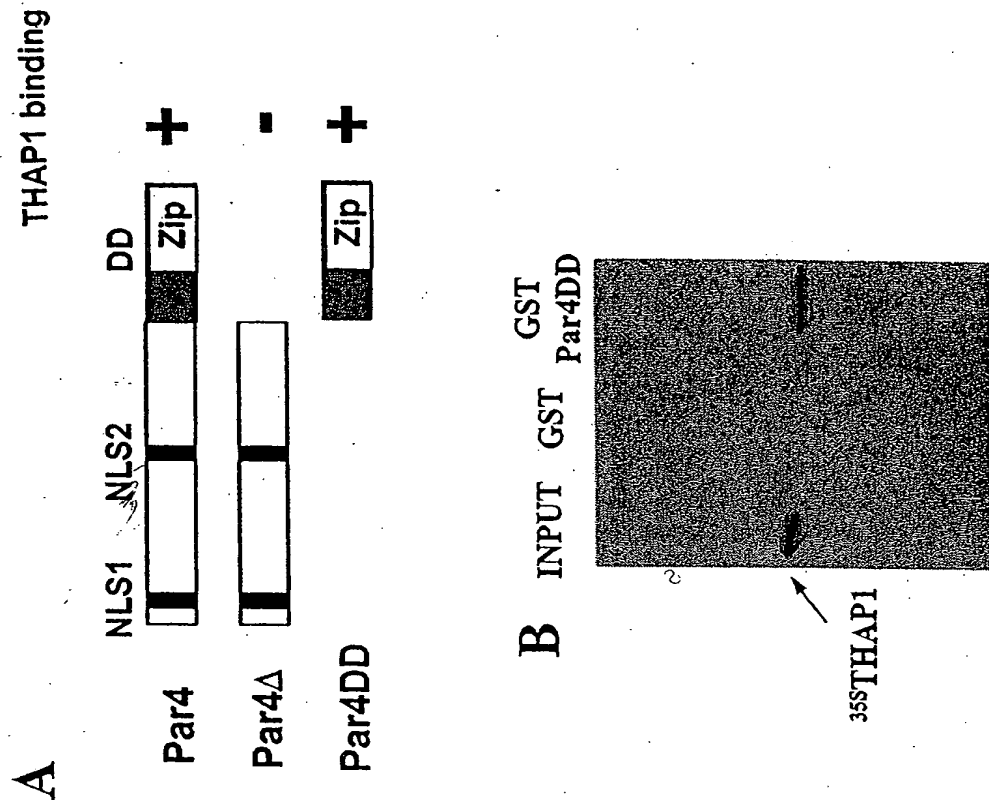
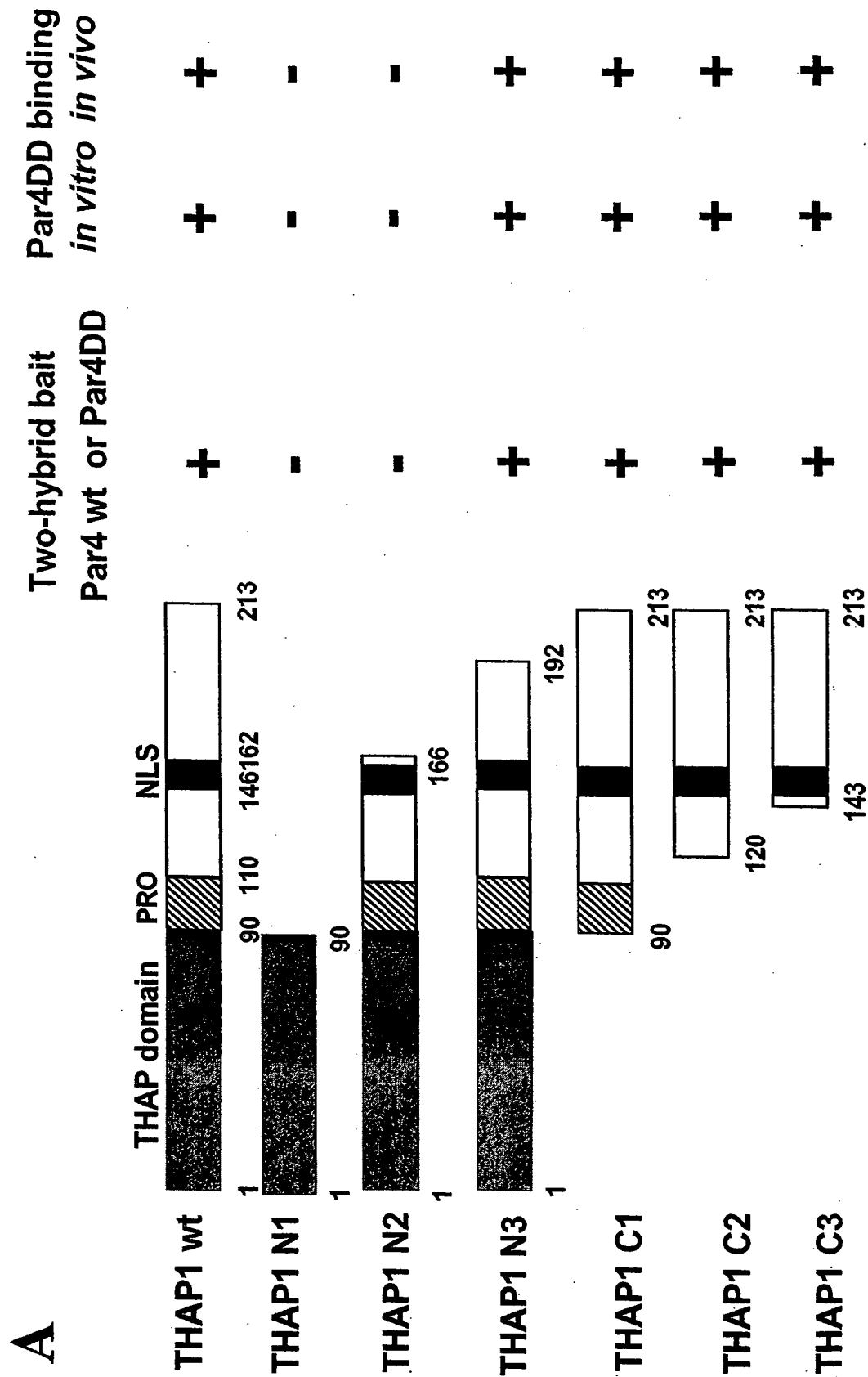


FIGURE 4A



**Figure 4b**

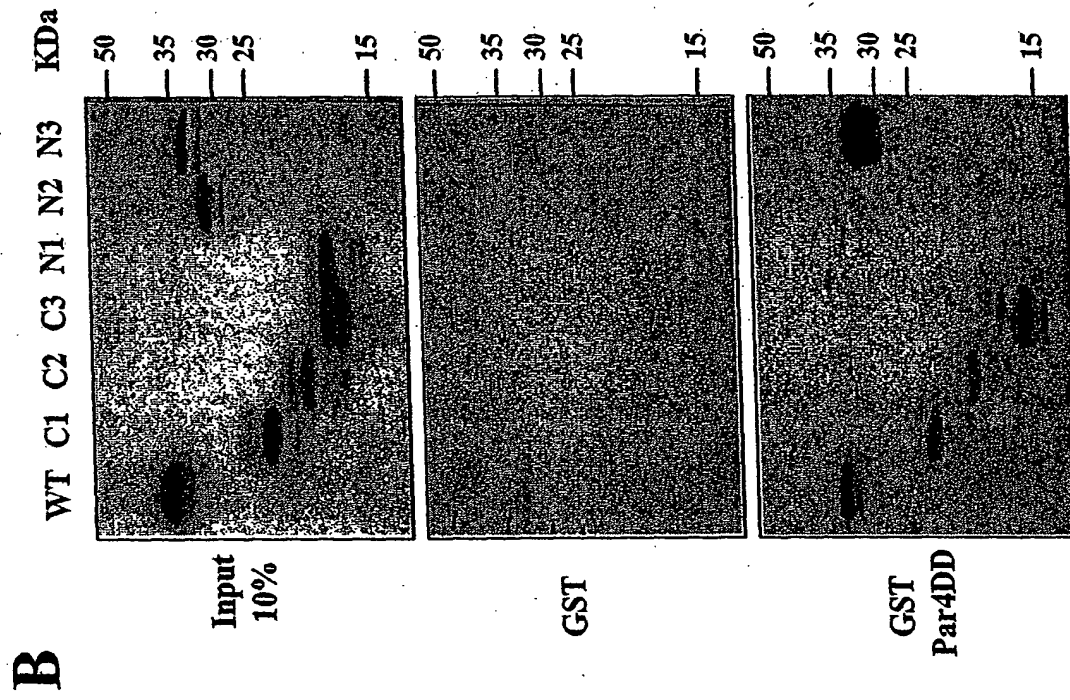


Figure 5

A

mZIP -VLEDVAAAEQGLREL--QRGRRCRERVCAALRAAAEQ**E**ARCRDG  
 mTHAP-1 -QLEQQVEKLRRKKLKTAAQRCRRQERQLEKLKEVVFQ**E**KDDASE  
 hTHAP-1 -QLEQQVEKLRRKKLKTAAQRCRRQERQLEKLKEVVFQ**E**KDDVSE

Consensus Par4 binding site: LE (X<sub>12-14</sub>) QRXRRQXR (X<sub>11</sub>) QXE

B

Two-hybrid bait  
 Par4 wt or Par4DD *in vitro* *in vivo*

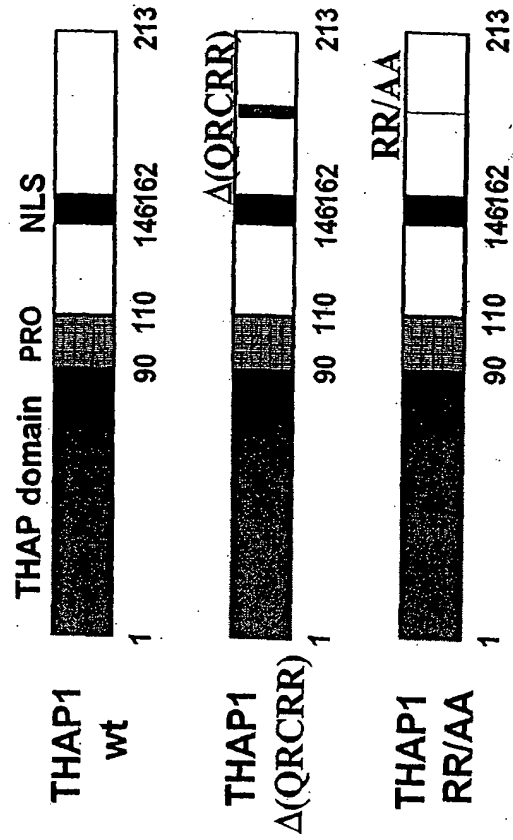


Figure 6

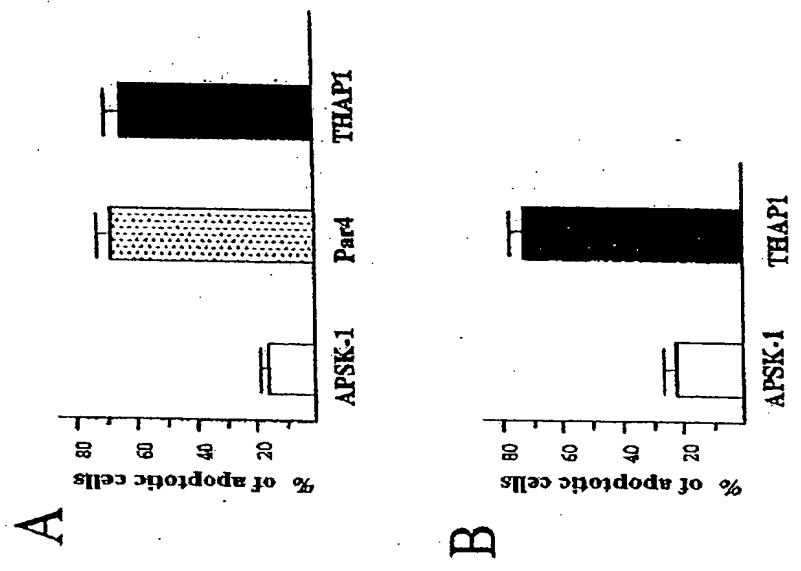


Figure 7

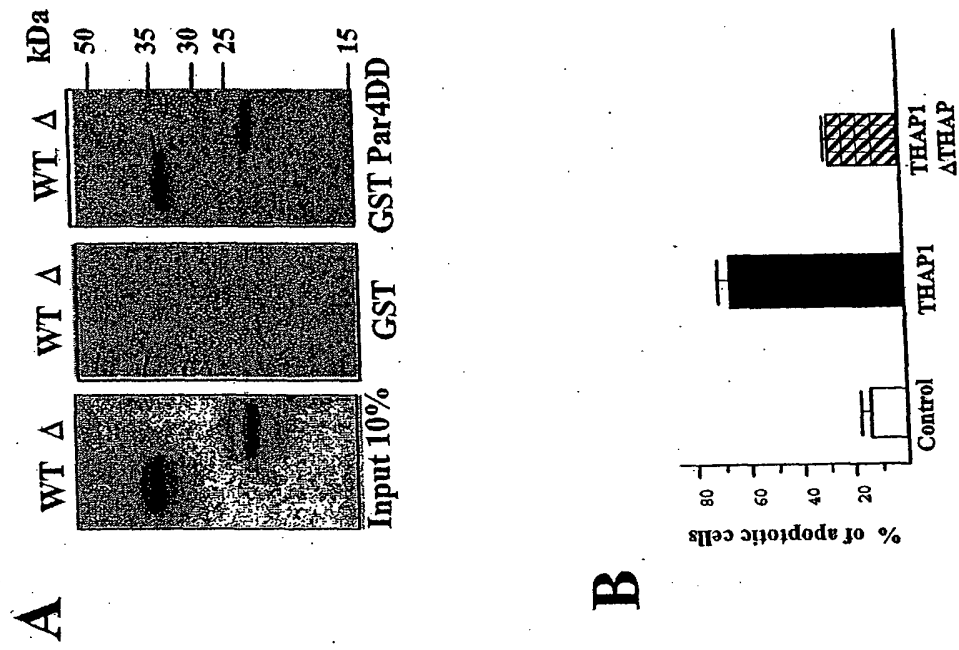




Figure 8

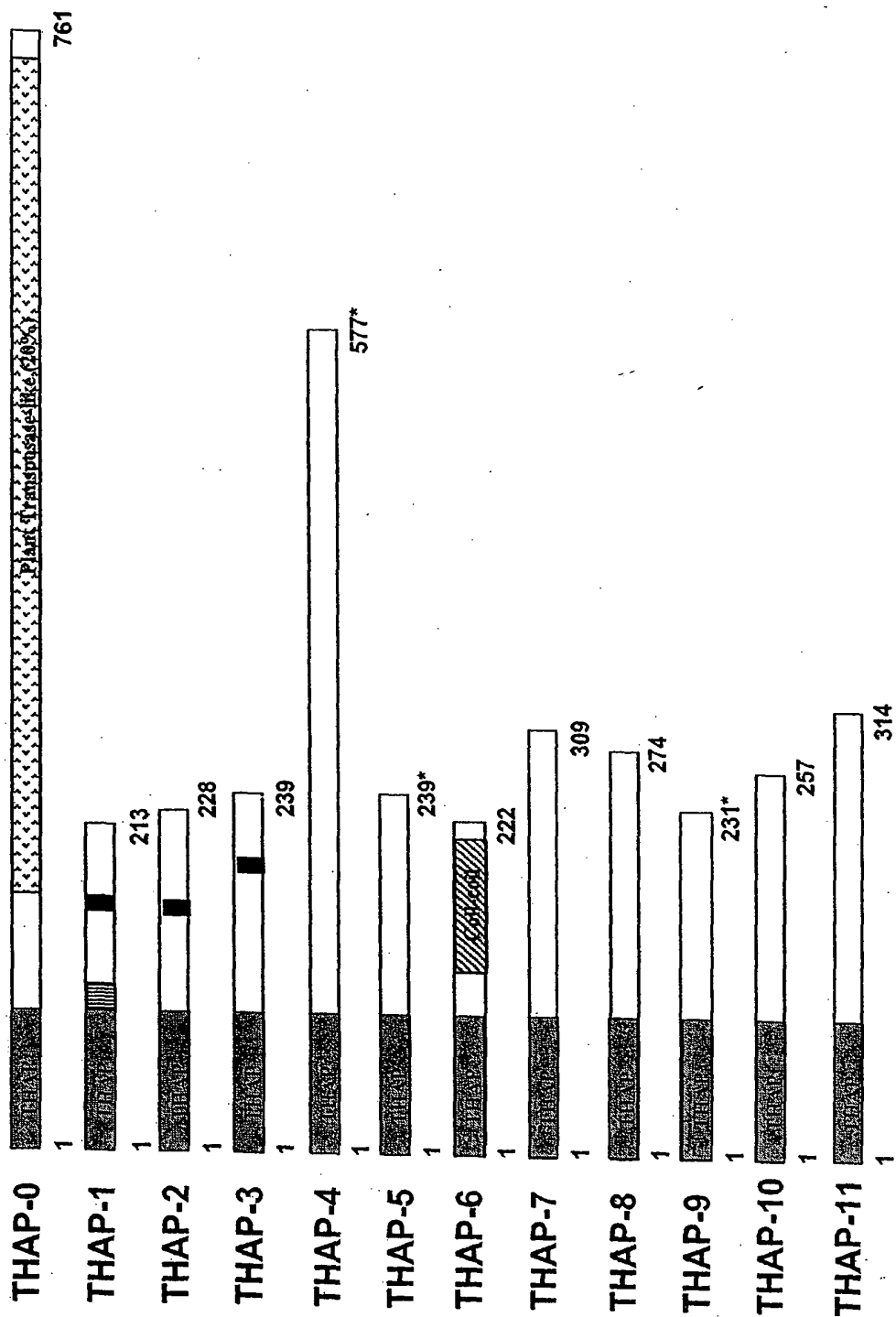


Figure 9

A

hTHAP1 1 **WV**SCSANGCKNRDYKDPVSEHFPPITRPSLOKMEAAVRRKNEKPKYSSISGSEHFTP  
dmTransposase 1 **WK**YIC-RECK-AVTGVTHHVPFCALRR---KMEQSLG---CSLGENSQLQDTHEND  
consensus 1 mv Cs y CKn K v K l Rpslck WE v rkn S lC HF

hTHAP1 61 **DO**ERK-----RECNNKLKENAVPTIFICTEPHDK  
dmTransposase 51 **SC**KAAAPAKGOTFKRRLNADAVEKVFHEPEPEKI  
consensus 61 fKaapakg k l AVpt l EP

B

hTHAP1 1 **WV**OS-SSVYCKNRDYD---KDPVSPFIKPLTRPSLCKMEAAVRR---RKN---EK  
hTHAP3 1 **WV**PS-SSARCCNNYSS---KQQLFHREFSRPELLKEMVING---RGN---EK  
hTHAP5 1 **WV**PK-SANICCKNRGRNKKD-RKISFYFTHHKKLEKIANKK-RDS---WV  
hTHAP8 1 **WV**Y-SAPICSATAGLIGADNRPSSEKPELKHGFLQAMFHOG-CEH---WV  
hTHAP4 1 **WV**IC-SAVNCSURQCK-GERASVFIHPELSDSLQIAFWO-SDN---WV  
hTHAP2 1 **WV**IN-SAACATYN---RHINSPFIHPELDPKREKAVRLR---RKN---WV  
hTHAP0 1 **WV**NT-SAMPNATRS---TOSDSEHREPR-PPARCKMENCN-RAD---LE  
hTHAP7 1 **WV**PR-SSACCCCTDRE-TNPEESFIHPEKDNPERGLANCO-RDPS-GOGIAD  
hTHAP9 1 **WV**RS-SNVGSTRDTVL-SREGESEHICEH-TDTQSKMIRAN-RVDPK-SKKIMI  
hTHAP6 1 **WV**C-SNICGASCLPN-SLKGHEHPEHLENER-KMILAK-RLDVN-AAGTIE  
hTHAP11 1 **WV**FTCCVPCVMNHS---RDMLEHFTFP-KIAELRLAKWS-RAGVSGCFSTGO  
hTHAP10 1 **WV**AR-SVAHCCNTTK---SGKLEHREPR-KRAVRLIDRVKCCAD---WV  
dmTransposase 1 **WV**X-SKFC-SKAVIG---KLIHPE-KALIKKIPEQSLG---CS---L  
consensus 1 mpk C a C nr k k vsfhkfp hd ir Wv v i W

hTHAP1 47 **P**-----TKYSSICSEHFTPDCKRECN-----NKLRENNAVPTIFICTEPHDK---  
hTHAP3 48 **P**-----KQHTVIGSEHREPECEASAGN-----RKNKRNNAVPTIFAFQDPTQ---  
hTHAP5 50 **P**-----SKYDFLCSHFTPDSLIDRWG-----IRKQTNVPTIFS-LFEDN---  
hTHAP8 51 **P**-----SCHOLCSHFTPSCQWRWG-----VRLRPDAVPSIGSGPPAK---  
hTHAP4 49 **P**-----TKYSFLCSHFTKDSSEKLEED---QHRLKMTAVPSIFH---LTEK---  
hTHAP2 46 **P**-----GKHTFLCSHREASCDITGO-----TR-RKMDNAVPTIFDFTHKSM---  
hTHAP0 45 **P**-----DKTPDLNKHRYLCAHFTSMICRTP-----YRTVIRONAVPTIFOLTS---  
hTHAP7 56 **P**-----SEYIFCSHPEEDCEBELGIS-----GYHEKECAVPTIESFS---  
hTHAP9 55 **P**-----FGAI-LCSHIFQDSIESYIGR-----EKKKCAVPSVSLYK---  
hTHAP6 55 **P**-----KGDV-LCSHIFKKTIDPSAEN-----IKMPPVPSIPSPYHLO---  
hTHAP11 54 **P**-----TTGHRFLCSHIFQGG-----KNTTVNAVPTIFPIRGVNERKV---  
hTHAP10 46 **G**-----NDRSVICSDHAPACPDVSSVI-----CKNLRFSSORLWAGAVPTLH---  
dmTransposase 38 **G**-----ENSQLCDTHENDSCAAAPAKGOTFKRRLNADAVEKVFHEPEPEKI---  
consensus 61 **P** ics HF f k k a v p t i f

hTHAP1	hTHAP2	hTHAP3	hTHAP4	hTHAP5	hTHAP6	hTHAP7	hTHAP8	hTHAP9	hTHAP10	hTHAP11	hTHAP12	hTHAP13	hTHAP14	hTHAP15	hTHAP16	hTHAP17	hTHAP18	hTHAP19	hTHAP20	hTHAP21	hTHAP22	hTHAP23	hTHAP24	hTHAP25	hTHAP26	hTHAP27	hTHAP28	hTHAP29	hTHAP30	hTHAP31	hTHAP32	hTHAP33	hTHAP34	hTHAP35	hTHAP36	hTHAP37	hTHAP38	hTHAP39	hTHAP40	hTHAP41	hTHAP42	hTHAP43	hTHAP44	hTHAP45	hTHAP46	hTHAP47	hTHAP48	hTHAP49	hTHAP50	hTHAP51	hTHAP52	hTHAP53	hTHAP54	hTHAP55	hTHAP56	hTHAP57	hTHAP58	hTHAP59	hTHAP60	hTHAP61	hTHAP62	hTHAP63	hTHAP64	hTHAP65	hTHAP66	hTHAP67	hTHAP68	hTHAP69	hTHAP70	hTHAP71	hTHAP72	hTHAP73	hTHAP74	hTHAP75	hTHAP76	hTHAP77	hTHAP78	hTHAP79	hTHAP80	hTHAP81	hTHAP82	hTHAP83	hTHAP84	hTHAP85	hTHAP86	hTHAP87	hTHAP88	hTHAP89	hTHAP90	hTHAP91	hTHAP92	hTHAP93	hTHAP94	hTHAP95	hTHAP96	hTHAP97	hTHAP98	hTHAP99	hTHAP100	hTHAP101	hTHAP102	hTHAP103	hTHAP104	hTHAP105	hTHAP106	hTHAP107	hTHAP108	hTHAP109	hTHAP110	hTHAP111	hTHAP112	hTHAP113	hTHAP114	hTHAP115	hTHAP116	hTHAP117	hTHAP118	hTHAP119	hTHAP120	hTHAP121	hTHAP122	hTHAP123	hTHAP124	hTHAP125	hTHAP126	hTHAP127	hTHAP128	hTHAP129	hTHAP130	hTHAP131	hTHAP132	hTHAP133	hTHAP134	hTHAP135	hTHAP136	hTHAP137	hTHAP138	hTHAP139	hTHAP140	hTHAP141	hTHAP142	hTHAP143	hTHAP144	hTHAP145	hTHAP146	hTHAP147	hTHAP148	hTHAP149	hTHAP150	hTHAP151	hTHAP152	hTHAP153	hTHAP154	hTHAP155	hTHAP156	hTHAP157	hTHAP158	hTHAP159	hTHAP160	hTHAP161	hTHAP162	hTHAP163	hTHAP164	hTHAP165	hTHAP166	hTHAP167	hTHAP168	hTHAP169	hTHAP170	hTHAP171	hTHAP172	hTHAP173	hTHAP174	hTHAP175	hTHAP176	hTHAP177	hTHAP178	hTHAP179	hTHAP180	hTHAP181	hTHAP182	hTHAP183	hTHAP184	hTHAP185	hTHAP186	hTHAP187	hTHAP188	hTHAP189	hTHAP190	hTHAP191	hTHAP192	hTHAP193	hTHAP194	hTHAP195	hTHAP196	hTHAP197	hTHAP198	hTHAP199	hTHAP200	hTHAP201	hTHAP202	hTHAP203	hTHAP204	hTHAP205	hTHAP206	hTHAP207	hTHAP208	hTHAP209	hTHAP210	hTHAP211	hTHAP212	hTHAP213	hTHAP214	hTHAP215	hTHAP216	hTHAP217	hTHAP218	hTHAP219	hTHAP220	hTHAP221	hTHAP222	hTHAP223	hTHAP224	hTHAP225	hTHAP226	hTHAP227	hTHAP228	hTHAP229	hTHAP230	hTHAP231	hTHAP232	hTHAP233	hTHAP234	hTHAP235	hTHAP236	hTHAP237	hTHAP238	hTHAP239	hTHAP240	hTHAP241	hTHAP242	hTHAP243	hTHAP244	hTHAP245	hTHAP246	hTHAP247	hTHAP248	hTHAP249	hTHAP250	hTHAP251	hTHAP252	hTHAP253	hTHAP254	hTHAP255	hTHAP256	hTHAP257	hTHAP258	hTHAP259	hTHAP260	hTHAP261	hTHAP262	hTHAP263	hTHAP264	hTHAP265	hTHAP266	hTHAP267	hTHAP268	hTHAP269	hTHAP270	hTHAP271	hTHAP272	hTHAP273	hTHAP274	hTHAP275	hTHAP276	hTHAP277	hTHAP278	hTHAP279	hTHAP280	hTHAP281	hTHAP282	hTHAP283	hTHAP284	hTHAP285	hTHAP286	hTHAP287	hTHAP288	hTHAP289	hTHAP290	hTHAP291	hTHAP292	hTHAP293	hTHAP294	hTHAP295	hTHAP296	hTHAP297	hTHAP298	hTHAP299	hTHAP300	hTHAP301	hTHAP302	hTHAP303	hTHAP304	hTHAP305	hTHAP306	hTHAP307	hTHAP308	hTHAP309	hTHAP310	hTHAP311	hTHAP312	hTHAP313	hTHAP314	hTHAP315	hTHAP316	hTHAP317	hTHAP318	hTHAP319	hTHAP320	hTHAP321	hTHAP322	hTHAP323	hTHAP324	hTHAP325	hTHAP326	hTHAP327	hTHAP328	hTHAP329	hTHAP330	hTHAP331	hTHAP332	hTHAP333	hTHAP334	hTHAP335	hTHAP336	hTHAP337	hTHAP338	hTHAP339	hTHAP340	hTHAP341	hTHAP342	hTHAP343	hTHAP344	hTHAP345	hTHAP346	hTHAP347	hTHAP348	hTHAP349	hTHAP350	hTHAP351	hTHAP352	hTHAP353	hTHAP354	hTHAP355	hTHAP356	hTHAP357	hTHAP358	hTHAP359	hTHAP360	hTHAP361	hTHAP362	hTHAP363	hTHAP364	hTHAP365	hTHAP366	hTHAP367	hTHAP368	hTHAP369	hTHAP370	hTHAP371	hTHAP372	hTHAP373	hTHAP374	hTHAP375	hTHAP376	hTHAP377	hTHAP378	hTHAP379	hTHAP380	hTHAP381	hTHAP382</
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[illegible]

Figure 10

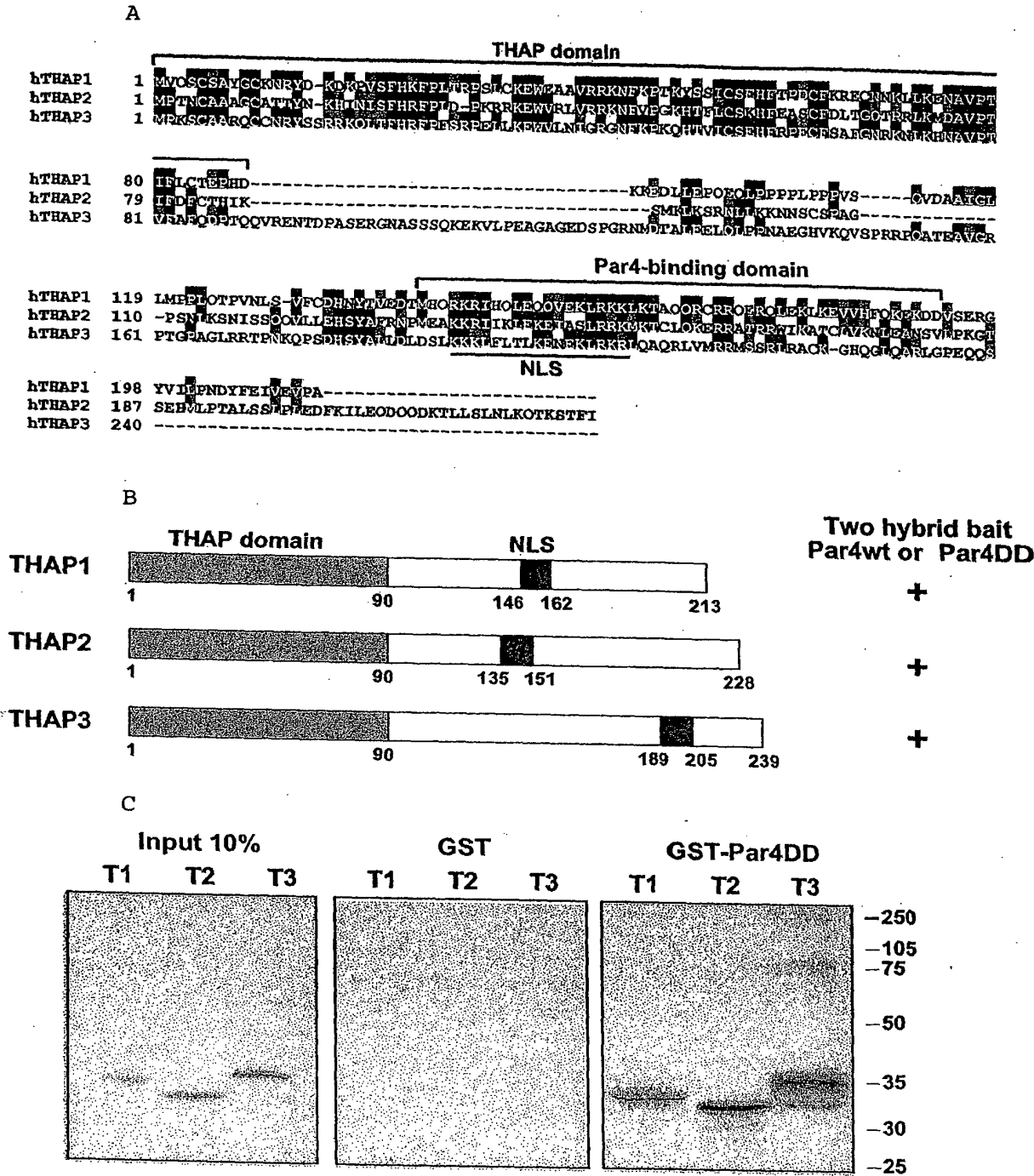


Figure 11

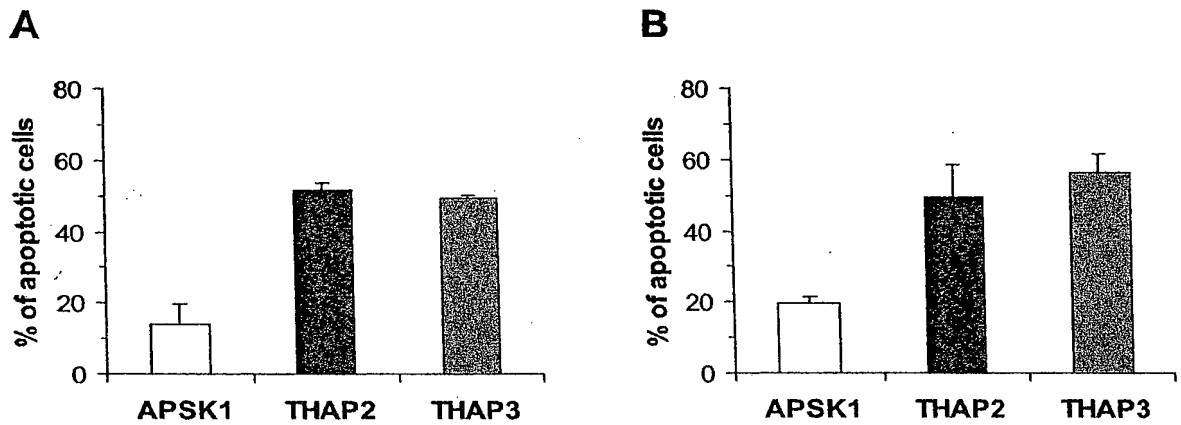


Figure 12

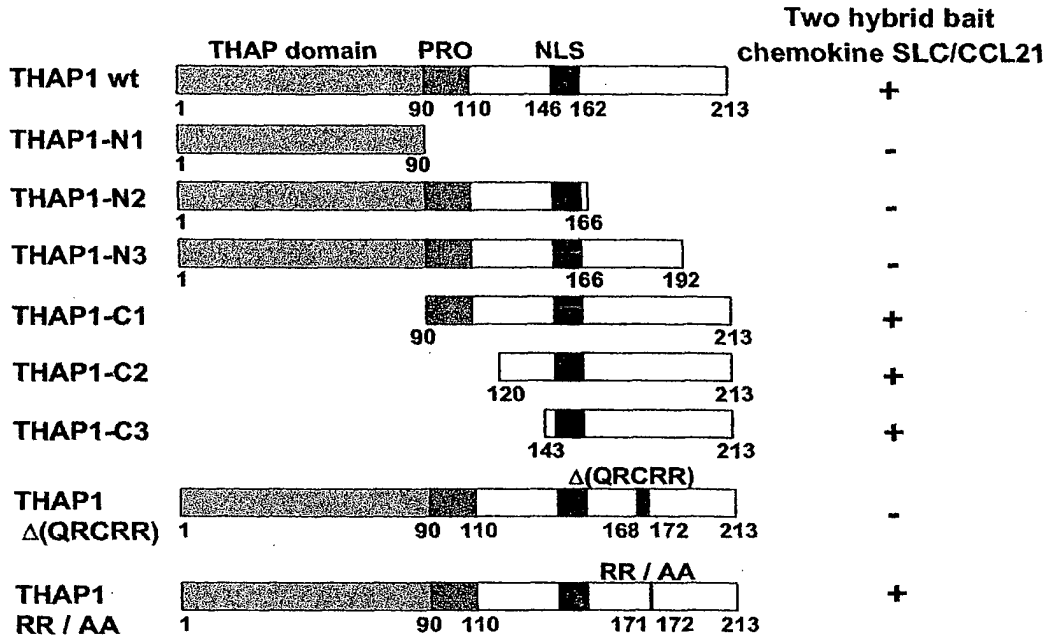
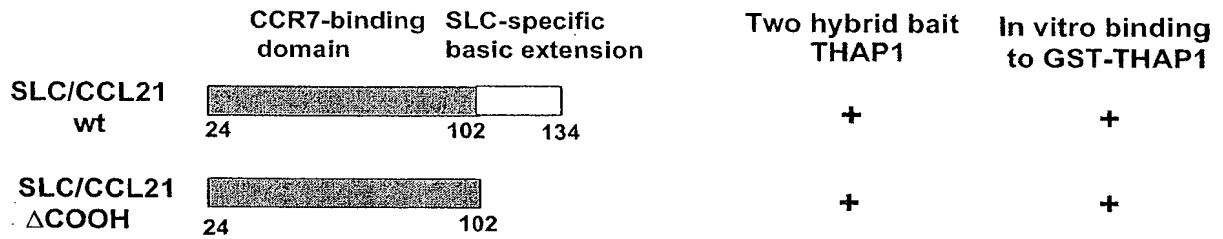


Figure 13





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06/19/03

FIGURE 14

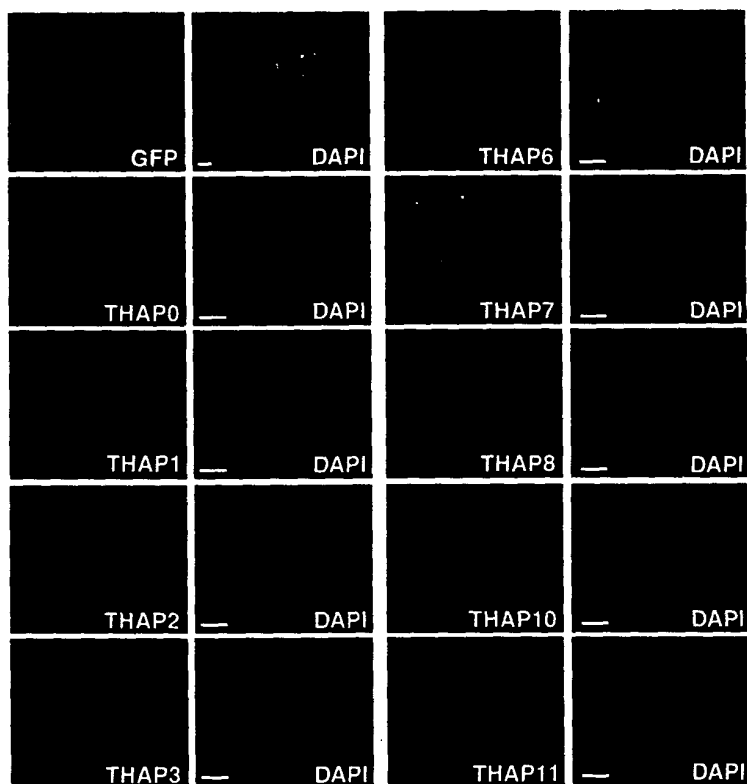


FIGURE 15

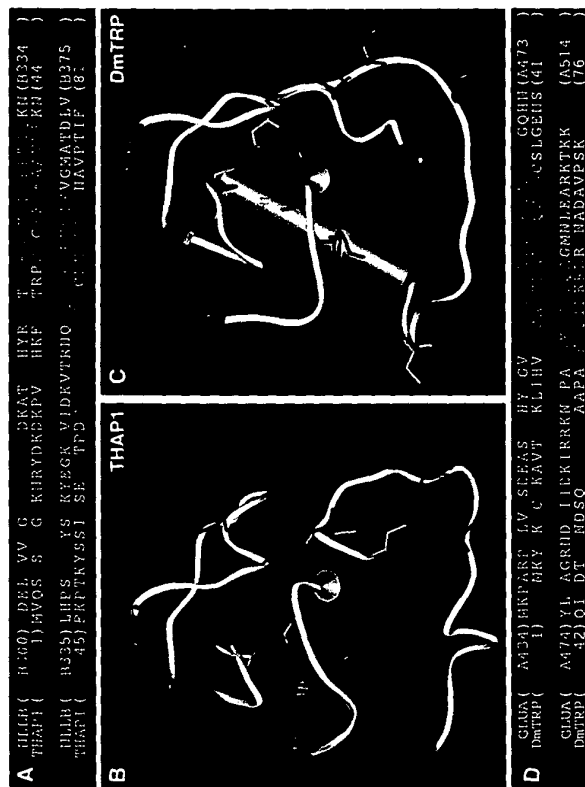


FIGURE 16

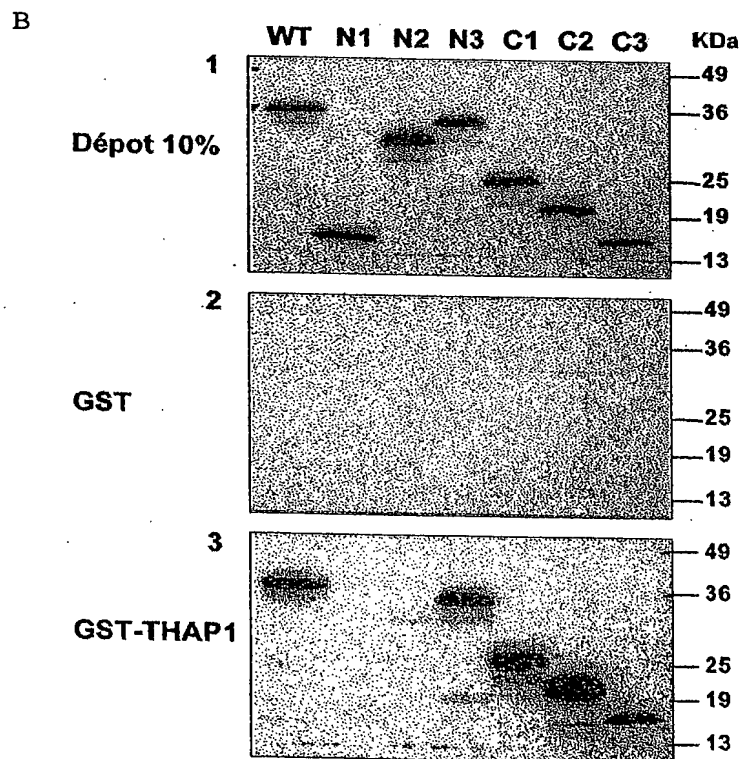
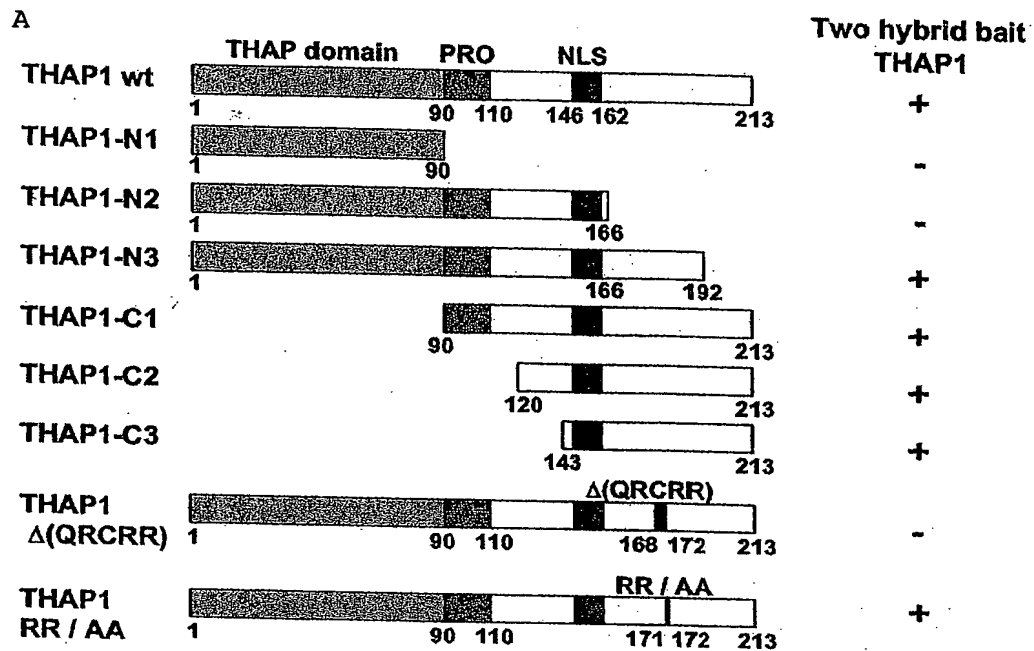


FIGURE 17

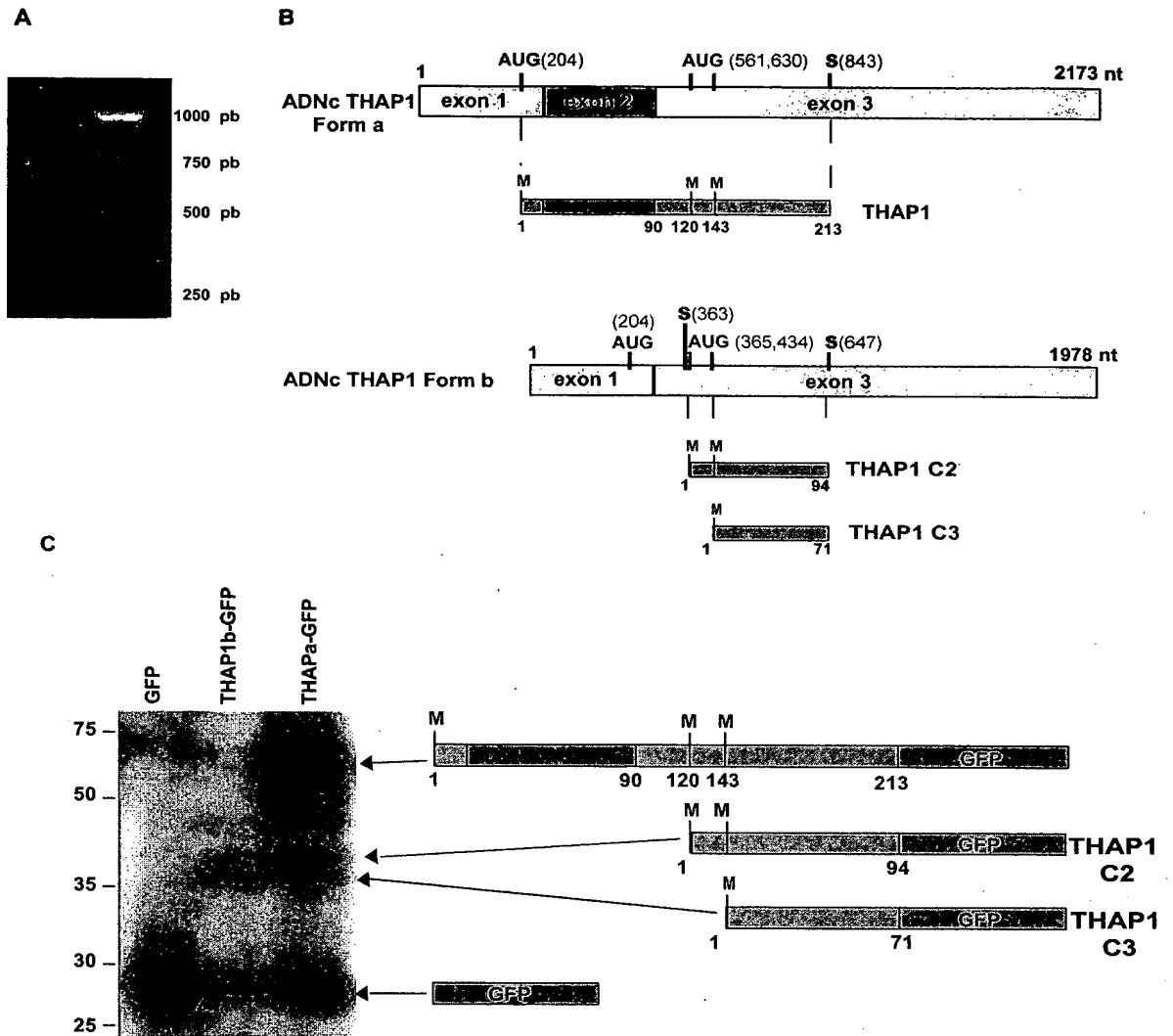


Figure 18

GGGCAT ACTAC TGGCAA  
GGGCAA ACTGT GGGCAT  
GGGCAT ACTAC TGGCAA  
GGGCAA ACTAC TGGCAA  
GGGCAA GTTCG TTGCAA  
GGGCAT GTAC TGGCAA  
GGGCAA CTGT GGGCAA  
GGGCAA CACTAC TGGCAA  
GGGCAA AGTAC TGGCAA

A

1) DR-5 Consensus Motif  
GGGCAAAnnnnnnTGGCAA  
(DR-4, DR-6)

TTGCCA GTACTAAGTGT GGGCAA  
CTGCCA GTACATAGTGT GGGCAA  
TTGCCA GTACTAAGTGT GGGCAA  
CTGCCA GTAGATACTGT GGGCAA  
TTGCCA GTAGTTAGGTGT GGGCGA  
TTGCCA GTAGTTAGTGT GGGCAA  
TTGCCA GTACCTACTAA GGGCAA  
TTGCCA GTAGTTAGTGT GGGCAG  
CTGCCA GTAGTAAGTGT GGGCAG

B

2) ER-11 Consensus Motif  
TTGCCAnnnnnnnnnnGGGCAA  
(ER-12)

Figure 19

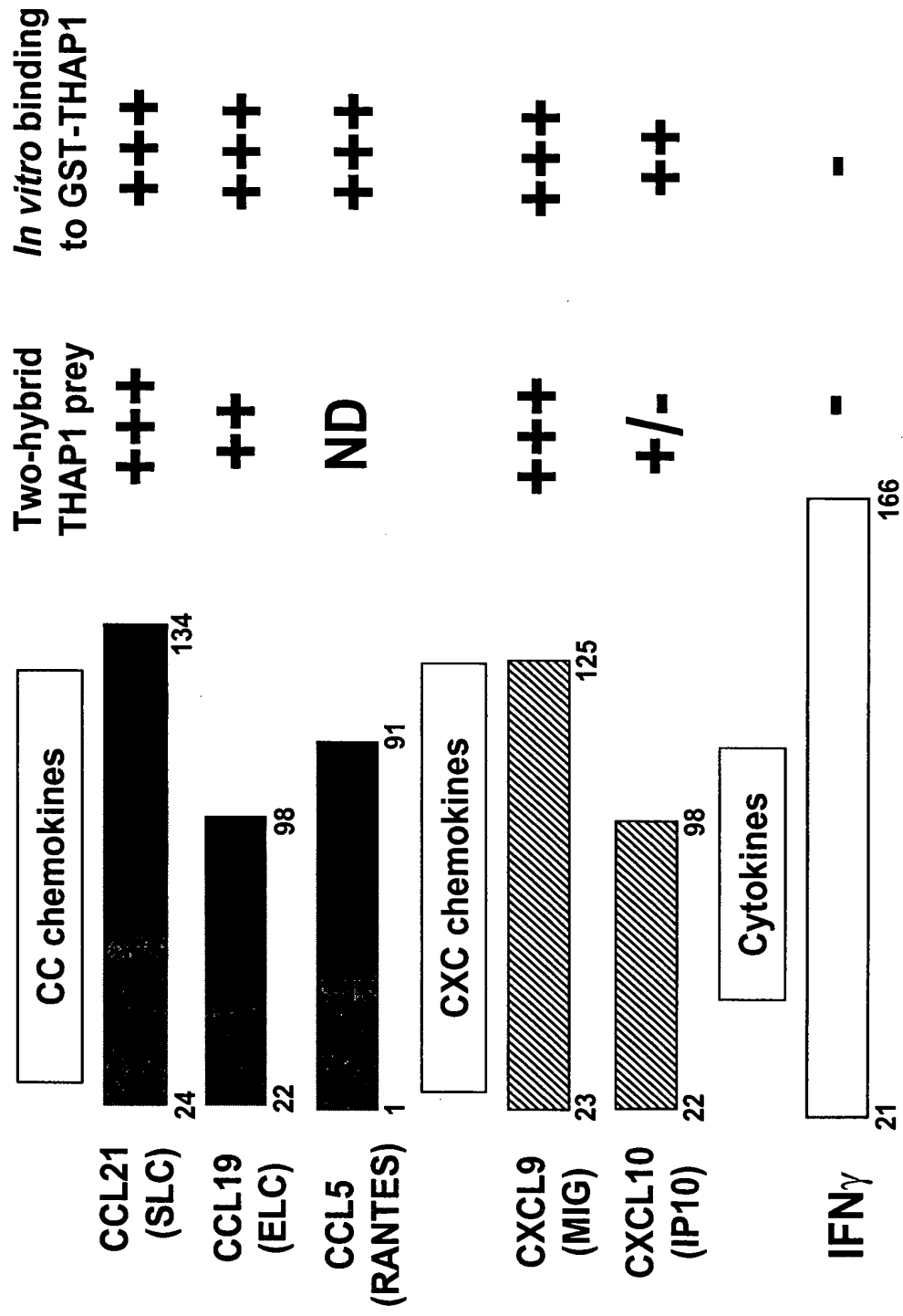


Figure 20

